

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Lal, Preeti  
Corley, Neil C.  
Tang, Y. Tom
- (ii) TITLE OF THE INVENTION: AUTOANTIGEN-LIKE PROTEIN
- (iii) NUMBER OF SEQUENCES: 3
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.  
(B) STREET: 3174 Porter Drive  
(C) CITY: Palo Alto  
(D) STATE: CA  
(E) COUNTRY: USA  
(F) ZIP: 94304
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Diskette  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: DOS  
(D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: To Be Assigned  
(B) FILING DATE: Herewith  
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER:  
(B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Billings, Lucy J.  
(B) REGISTRATION NUMBER: 36,749  
(C) REFERENCE/DOCKET NUMBER: PF-0385 US
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: 650-855-0555  
(B) TELEFAX: 650-845-4166  
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 395 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:  
(A) LIBRARY: HUVENOB01  
(B) CLONE: 35842

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Phe	Pro	Arg	Val	Ser	Thr	Phe	Leu	Pro	Leu	Arg	Pro	Leu	Ser	Arg	1	5	10	15
His	Pro	Leu	Ser	Ser	Gly	Ser	Pro	Glu	Thr	Ser	Ala	Ala	Ala	Ile	Met	20	25	30	
Leu	Leu	Thr	Val	Arg	His	Gly	Thr	Val	Arg	Tyr	Arg	Ser	Ser	Ala	Leu	35	40	45	
Leu	Ala	Arg	Thr	Lys	Asn	Asn	Ile	Gln	Arg	Tyr	Phe	Gly	Thr	Asn	Ser	50	55	60	
Val	Ile	Cys	Ser	Lys	Lys	Asp	Lys	Gln	Ser	Val	Arg	Thr	Glu	Glu	Thr	65	70	75	80
Ser	Lys	Glu	Thr	Ser	Glu	Ser	Gln	Asp	Ser	Glu	Lys	Glu	Asn	Thr	Lys	85	90	95	
Lys	Asp	Leu	Leu	Gly	Ile	Ile	Lys	Gly	Met	Lys	Val	Glu	Leu	Ser	Thr	100	105	110	
Val	Asn	Val	Arg	Thr	Thr	Lys	Pro	Pro	Lys	Arg	Arg	Pro	Leu	Lys	Ser	115	120	125	
Leu	Glu	Ala	Thr	Leu	Gly	Arg	Leu	Arg	Arg	Ala	Thr	Glu	Tyr	Ala	Pro	130	135	140	
Lys	Lys	Arg	Ile	Glu	Pro	Leu	Ser	Pro	Glu	Leu	Val	Ala	Ala	Ala	Ser	145	150	155	160
Ala	Val	Ala	Asp	Ser	Leu	Pro	Phe	Asp	Lys	Gln	Thr	Thr	Lys	Ser	Glu	165	170	175	
Leu	Leu	Ser	Gln	Leu	Gln	Gln	His	Glu	Glu	Glu	Ser	Arg	Ala	Gln	Arg	180	185	190	
Asp	Ala	Lys	Arg	Pro	Lys	Ile	Ser	Phe	Ser	Asn	Ile	Ile	Ser	Asp	Met	195	200	205	
Lys	Val	Ala	Arg	Ser	Ala	Thr	Ala	Arg	Val	Arg	Ser	Arg	Pro	Glu	Leu	210	215	220	
Arg	Ile	Gln	Phe	Asp	Glu	Gly	Tyr	Asp	Asn	Tyr	Pro	Gly	Gln	Glu	Lys	225	230	235	240
Thr	Asp	Asp	Leu	Lys	Lys	Arg	Lys	Asn	Ile	Phe	Thr	Gly	Lys	Arg	Leu	245	250	255	
Asn	Ile	Phe	Asp	Met	Met	Ala	Val	Thr	Lys	Glu	Ala	Pro	Glu	Thr	Asp	260	265	270	
Thr	Ser	Pro	Ser	Leu	Trp	Asp	Val	Glu	Phe	Ala	Lys	Gln	Leu	Ala	Thr	275	280	285	
Val	Asn	Glu	Gln	Pro	Leu	Gln	Asn	Gly	Phe	Glu	Glu	Leu	Ile	Gln	Trp	290	295	300	
Thr	Lys	Glu	Gly	Lys	Leu	Trp	Glu	Phe	Pro	Ile	Asn	Asn	Glu	Ala	Gly	305	310	315	320
Phe	Asp	Asp	Asp	Gly	Ser	Glu	Phe	His	Glu	His	Ile	Phe	Leu	Glu	Lys	325	330	335	
His	Leu	Glu	Ser	Phe	Pro	Lys	Gln	Gly	Pro	Ile	Arg	His	Phe	Met	Glu	340	345	350	
Leu	Val	Thr	Cys	Gly	Leu	Ser	Lys	Asn	Pro	Tyr	Leu	Ser	Val	Lys	Gln	355	360	365	
Lys	Val	Glu	His	Ile	Glu	Trp	Phe	Arg	Asn	Tyr	Phe	Asn	Glu	Lys	Lys	370	375	380	
Asp	Ile	Leu	Lys	Glu	Ser	Asn	Ile	Gln	Phe	Asn						385	390	395	

## (2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1314 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
 (A) LIBRARY: HUVENOB01  
 (B) CLONE: 35842

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GACGTGTTTG	GCAGCGGGAC	GCACCATTTTC	AGTTGTGTTC	TTGGTTCATT	TCGTGTCTCG	60
GCGATGTTTC	CTAGAGTCTC	GACGTTCCCTA	CCTCTTCGCC	CCCTTTCCCG	CCACCCTTTG	120
TCCTCTGGAA	GCCCGGAGAC	ATCAGCGGCT	GCGATTATGC	TACTCACTGT	TCGGCACGGA	180
ACAGTCAGGT	ACCGCAGTTC	AGCGCTGTTG	GCCCGGACAA	AAAATAACAT	CCAAAGATAT	240
TTTGGCACTA	ACAGTGTGAT	CTGTAGCAAG	AAAGATAAGC	AGTCTGTTCG	AACTGAGGAG	300
ACTTCCAAGG	AGACTTCAGA	GAGCCAAGAC	AGTGAAAAGG	AAAATACGAA	AAAAGACTTG	360
TTAGGCATTA	TAAAGGGCAT	GAAAGTTGAA	TTAAGCACAG	TAAATGTACG	AACAACAAAG	420
CCCCCAAAA	GAAGACCACT	TAAAAGTTTG	GAAGCTACAC	TTGGCAGGCT	TCGAAGAGCT	480
ACAGAATATG	CTCCAAAGAA	GAGAATTGAG	CCCCTGAGTC	CTGAGTTGGT	GGCAGCTGCA	540
TCTGCTGTGG	CAGATTCTCT	CCCTTTTGAT	AAGCAAAACA	CCAAGTCAGA	GCTGCTGAGC	600
CAGCTCCAGC	AGCATGAGGA	AGAGTCAAGG	GCACAGAGAG	ATGCAAAGCG	ACCTAAAATT	660
AGTTTCAGTA	ACATAATATC	AGATATGAAA	GTTGCCAGAT	CTGCTACAGC	TAGAGTTCGT	720
TCAAGACCAG	AGCTTCGGAT	TCAGTTTGAT	GAAGGCTATG	ACAATTATCC	TGGCCAGGAG	780
AAGACGGATG	ATCTTAAAAA	AAGGAAAAAT	ATATTCACAG	GGAAAAGACT	TAATATTTTT	840
GACATGATGG	CAGTTACTAA	AGAAGCACCT	GAAACAGACA	CATCACCTTC	ACTTTGGGAT	900
GTGGAATTTG	CTAAGCAGTT	AGCCACAGTA	AATGAACAAC	CCCTTCAGAA	TGGATTTGAA	960
GAGCTGATCC	AGTGGACAAA	AGAGGGGAAA	CTATGGGAGT	TCCCAATTAA	CAATGAAGCA	1020
GGTTTTGATG	ATGATGGTTC	AGAATTTTCAT	GAACATATAT	TTCTGGAGAA	ACACCTGGAG	1080
AGCTTTCCAA	AACAAGGACC	AATTCGCCAC	TTCATGGAGC	TGGTGACTTG	TGGCCTTTCC	1140
AAAAACCCAT	ATCTTAGTGT	TAAACAGAAG	GTTGAACACA	TAGAGTGGTT	TAGAAATTAT	1200
TTTAATGAAA	AAAAGGATAT	TCTAAAAGAA	AGTAACATAC	AGTTCAATTA	AGACCATGGA	1260
AATTTTATTT	TCAAACAATT	AGAGATGGAT	ATTACAACATA	AATAAAATAA	TTGC	1314

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 384 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
 (A) LIBRARY: GenBank  
 (B) CLONE: 1272669

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Leu	His	Arg	Ile	Pro	Ala	Phe	Leu	Arg	Pro	Arg	Pro	Phe	Ser	Gly
1				5				10					15		
Leu	Pro	Leu	Ser	Cys	Gly	Asn	Arg	Asp	Val	Ser	Val	Ala	Val	Leu	Pro
			20					25				30			
Ala	Ala	Gln	Ser	Gly	Ala	Val	Arg	Thr	Glu	Asn	Asn	Ile	Gln	Arg	His
		35					40					45			
Phe	Cys	Thr	Ser	Arg	Ser	Ile	Cys	Ser	Lys	Lys	Val	Asp	Gln	Ser	Val
	50					55					60				
Pro	Ala	Asn	Glu	Ile	Ser	Gln	Lys	Ala	Ala	Glu	Ser	Gln	Gly	Arg	Gly
65						70				75				80	
Lys	Glu	Thr	Leu	Lys	Lys	Asp	Leu	Leu	Asp	Ile	Ile	Lys	Asp	Met	Lys
			85						90					95	
Val	Asp	Leu	Ser	Thr	Ala	Asn	Val	Lys	Thr	Pro	Lys	Pro	Arg	Gly	Arg
			100					105					110		
Lys	Pro	Ser	Ala	Ser	Leu	Glu	Ala	Thr	Val	Asp	Arg	Leu	Gln	Lys	Ala
		115					120					125			
Pro	Glu	Asp	Pro	Pro	Lys	Lys	Arg	Asn	Glu	Phe	Leu	Ser	Pro	Glu	Leu

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130		135		140											
Val	Ala	Ala	Ser	Ala	Val	Ala	Asp	Ser	Leu	Pro	Phe	Asp	Lys	Gln	
145		150		155										160	
Thr	Thr	Lys	Ser	Glu	Leu	Leu	Arg	Gln	Leu	Gln	Gln	His	Glu	Glu	Glu
		165		170										175	
Leu	Arg	Ala	Gln	Lys	Asp	Arg	Glu	Lys	Arg	Arg	Ile	Ser	Phe	Thr	His
		180		185										190	
Ile	Ile	Ser	Asn	Met	Lys	Ile	Ala	Lys	Ser	Pro	Ser	Gly	Arg	Ala	Ser
		195		200										205	
Thr	Arg	Pro	Gln	His	Gln	Ile	Gln	Phe	Asp	Glu	Asp	Met	Asp	Ser	Ser
		210		215										220	
Leu	Lys	Gln	Glu	Lys	Pro	Thr	Asp	Phe	Arg	Lys	Arg	Lys	Tyr	Leu	Phe
225		230		235										240	
Lys	Gly	Lys	Arg	Leu	Ser	Ile	Phe	Ala	Asp	Lys	Ala	Phe	Ala	Asp	Glu
		245		250										255	
Pro	Pro	Glu	Pro	Glu	Ala	Ser	Pro	Ser	Leu	Trp	Glu	Ile	Glu	Phe	Ala
		260		265										270	
Lys	Gln	Leu	Ala	Ser	Val	Ala	Asp	Gln	Pro	Phe	Glu	Asn	Gly	Phe	Glu
		275		280										285	
Glu	Met	Ile	Gln	Trp	Thr	Lys	Glu	Gly	Lys	Leu	Trp	Glu	Phe	Pro	Val
290		295		300											
Asn	Asn	Glu	Ala	Gly	Leu	Asp	Asp	Asp	Gly	Ser	Glu	Phe	His	Glu	His
305		310		315										320	
Ile	Phe	Leu	Asp	Lys	Tyr	Leu	Glu	Asp	Phe	Pro	Lys	Gln	Gly	Pro	Ile
		325		330										335	
Arg	Leu	Phe	Met	Glu	Leu	Val	Thr	Cys	Gly	Leu	Ser	Lys	Asn	Pro	Tyr
		340		345										350	
Leu	Ser	Val	Lys	Gln	Lys	Val	Glu	His	Ile	Glu	Trp	Phe	Arg	Asn	Tyr
		355		360										365	
Phe	Asn	Glu	Lys	Arg	Asp	Ile	Leu	Lys	Glu	Asn	Asn	Ile	Ala	Phe	Thr
370		375		380											